

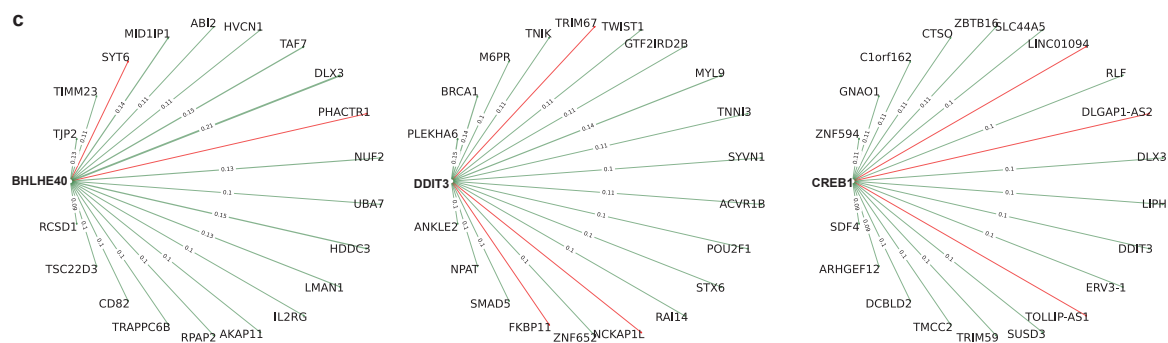
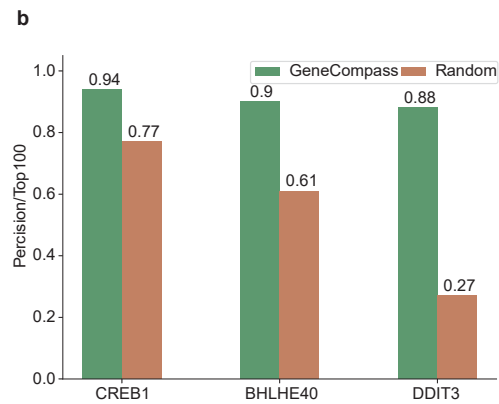
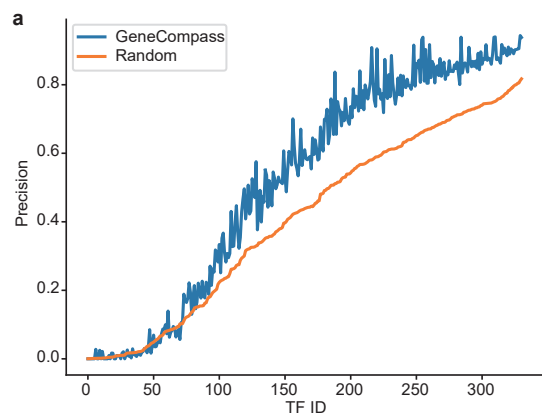


Fig. S4| Evaluation on GeneCompass's ability in GRN recognition. **a**, Comparison of GRN inference accuracy between GeneCompass (*in silico* deletion) and random sampling. **b**, Comparison of precision for the top 100 most likely predicted target genes (TGs) between GeneCompass and random selection after perturbing CREB1, BLHE40, and DDIT3, which intersected with the ChIP-Atlas ground-truth data. **c**, Illustration of the top 20 most likely TGs predicted by GeneCompass after perturbing CREB1, BLHE40, and DDIT3, with 17, 18, and 17 genes overlapping with TGs identified for each TF in ChIP-Atlas. Green lines indicate correct predictions, while red lines indicate incorrect predictions.